

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Screening Method

<130> P04-080PCT

<150> JP 2002-3769

<151> 2002-01-10

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Partial amino acid sequence of Egr-1 protein which is conserved between human, mouse and rat.

<400> 1

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Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His
          35          40          45
Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
          50          55          60
Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His
65          70          75          80
Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
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Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys
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<210> 2

<211> 543

<212> PRT

<213> Homo sapiens

<400> 2

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Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
          35          40          45
Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
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Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65          70          75          80
Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
          85          90          95
Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
          100          105          110
Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu

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Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
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Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
165      170      175
Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
180      185      190
Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
195      200      205
Phe Pro Thr Pro Asn Thr Asp Ile Phe Pro Glu Pro Gln Ser Gln Ala
210      215      220
Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225      230      235      240
Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
245      250      255
Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
260      265      270
Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
275      280      285
Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
290      295      300
Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg
305      310      315      320
Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
325      330      335
Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
340      345      350
Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
355      360      365
Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr
370      375      380
Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385      390      395      400
Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys
405      410      415
Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
420      425      430
Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
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Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr
450      455      460
Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
465      470      475      480
Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
485      490      495
Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
500      505      510
Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
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Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys
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<210> 3
<211> 1629
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)..(1629)
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tct gac ccg ttc gga tcc ttt cct cac tcg ccc acc atg gac aac tac	96
Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr	
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cct aag ctg gag gag atg atg ctg ctg agc aac ggg gct ccc cag ttc	144
Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe	
35 40 45	
ctc ggc gcc gcc ggg gcc cca gag ggc agc ggc agc aac agc agc agc	192
Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser	
50 55 60	
agc agc agc ggg ggc ggt gga ggc ggc ggg ggc ggc agc aac agc agc	240
Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser	
65 70 75 80	
agc agc agc agc acc ttc aac cct cag gcg gac acg ggc gag cag ccc	288
Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro	
85 90 95	
tac gag cac ctg acc gca gag tct ttt cct gac atc tct ctg aac aac	336
Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn	
100 105 110	
gag aag gtg ctg gtg gag acc agt tac ccc agc caa acc act cga ctg	384
Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu	
115 120 125	
ccc ccc atc acc tat act ggc cgc ttt tcc ctg gag cct gca ccc aac	432
Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn	
130 135 140	
agt ggc aac acc ttg tgg ccc gag ccc ctc ttc agc ttg gtc agt ggc	480
Ser Gly Asn Thr Leu Trp Pro Glu Pro Leu Phe Ser Leu Val Ser Gly	
145 150 155 160	
cta gtg agc atg acc aac cca ccg gcc tcc tcg tcc tca gca cca tct	528
Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser	
165 170 175	
cca gcg gcc tcc tcc gcc tcc gcc tcc cag agc cca ccc ctg agc tgc	576
Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys	
180 185 190	
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Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr	
195 200 205	
ttc ccc acg ccg aac act gac att ttc cct gag cca caa agc cag gcc	672
Phe Pro Thr Pro Asn Thr Asp Ile Phe Pro Glu Pro Gln Ser Gln Ala	
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Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr	
225 230 235 240	
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Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu	
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Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys	
260 265 270	
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Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro	
275 280 285	
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Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu	
290 295 300	
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Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg	
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04080seq.txt

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355 360 365
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Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr
370 375 380
acc cac atc cgc acc cac aca ggc gaa aag ccc ttc gcc tgc gac atc 1200
Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385 390 395 400
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Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys
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atc cac ttg cgg cag aag gac aag aaa gac aca agt gtt gtg gcc 1296
Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
420 425 430
tct tcg gcc acc tcc tct ctc tct tcc tac ccg tcc ccg gtt gct acc 1344
Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
435 440 445
tct tac ccg tcc ccg gtt act acc tct tat cca tcc ccg gcc acc acc 1392
Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr
450 455 460
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Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
465 470 475 480
acc tac cca tcc cct gtg cac agt ggc ttc ccc tcc ccg tcg gtg gcc 1488
Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
485 490 495
acc acg tac tcc tct gtt ccc cct gct ttc ccg gcc cag gtc agc agc 1536
Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
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Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
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<210> 4
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Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
20 25 30
cct aag ctg gag gag atg atg ctg ctg agc aac ggg gct ccc cag ttc 144
Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
35 40 45
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Ser	Ser	Ser	Ser	Thr	Phe	Asn	Pro	Gln	Ala	Asp	Thr	Gly	Glu	Gln	Pro		
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tac	gag	cac	ctg	acc	gca	gag	tct	ttt	cct	gac	atc	tct	ctg	aac	aac	336	
Tyr	Glu	His	Leu	Thr	Ala	Glu	Ser	Phe	Pro	Asp	Ile	Ser	Leu	Asn	Asn		
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gag	aag	gtg	ctg	gtg	gag	acc	agt	tac	ccc	agc	caa	acc	act	cga	ctg	384	
Glu	Lys	Val	Leu	Val	Glu	Thr	Ser	Tyr	Pro	Ser	Gln	Thr	Thr	Arg	Leu		
				115				120						125			
ccc	ccc	atc	acc	tat	act	ggc	cgc	ttt	tcc	ctg	gag	cct	gca	ccc	aac	432	
Pro	Pro	Ile	Thr	Tyr	Thr	Gly	Arg	Phe	Ser	Leu	Glu	Pro	Ala	Pro	Asn		
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Ser	Gly	Asn	Thr	Leu	Trp	Pro	Glu	Pro	Leu	Phe	Ser	Leu	Val	Ser	Gly		
				145				150						155			
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Leu	Val	Ser	Met	Thr	Asn	Pro	Pro	Ala	Ser	Ser	Ser	Ser	Ala	Pro	Ser		
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Pro	Tyr	Ala	Cys	Pro	Val	Glu	Ser	Cys	Asp	Arg	Arg	Phe	Ser	Arg	Ser		
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465										470										475										480										
acc	tac	cca	tcc	cct	gtg	cac	agt	ggc	ttc	ccc	tcc	ccg	tcg	gtg	gcc		1488																							
Thr	Tyr	Pro	Ser	Pro	Val	His	Ser	Gly	Phe	Pro	Ser	Pro	Ser	Val	Ala																									
485										490										495																				
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Phe	Pro	Ser	Ser	Ala	Val	Thr	Asn	Ser	Phe	Ser	Ala	Ser	Thr	Gly	Leu																									
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<213> Artificial

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<221> misc_feature

<223> Oligonucleotide designed to act as decoy for Egr-1.

<400> 5

gcgtgggcg

9

<210> 6

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gcgggggcg

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<210> 7

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<223> Oligonucleotide designed to act as antisense DNA for Egr-1 mRNA.

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20

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cDNA.

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cDNA.

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DNA capable of binding with Egr-1.

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DNA incapable of binding with Egr-1.

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